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Application Serial Number: 09/989,025
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TECH CENTER 1600/2900

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PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

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Revised 01/29/2002



1646

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/989,025

DATE: 02/19/2002

TIME: 11:52:11

MAR -5 2002

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\02192002\I989025.raw

p.4 TECH CENTER 1600/2900

3 <110> APPLICANT: NAKAI, JUNICHI
 5 <120> TITLE OF INVENTION: METHOD FOR PRODUCING A BIOSENSOR PROTEIN CAPABLE OF
 REGULATING A
 6 FLUORESCENCE PROPERTY OF GREEN FLUORESCENT PROTEIN, AND THE BIOSENSOR PROTEIN
 7 PRODUCED BY THE METHOD
 9 <130> FILE REFERENCE: 216339US0
 11 <140> CURRENT APPLICATION NUMBER: 09/989,025
 12 <141> CURRENT FILING DATE: 2001-11-21
 14 <150> PRIOR APPLICATION NUMBER: JP/2000-356047
 15 <151> PRIOR FILING DATE: 2000-11-22
 17 <160> NUMBER OF SEQ ID NOS: 17
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 717
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Aequorea victoria
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (1)..(717)
 29 <223> OTHER INFORMATION:
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 35 1 5 10 15
 37 gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc gag 96
 38 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 39 20 25 30
 41 ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc 144
 42 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 43 35 40 45
 45 acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg 192
 46 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
 47 50 55 60
 49 acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag cag 240
 50 Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 51 65 70 75 80
 53 cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc 288
 54 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 55 85 90 95
 57 acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag gtg 336
 58 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 59 100 105 110
 61 aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc atc 384
 62 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile

Does Not Comply
 Corrected Diskette Needed

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Input Set : A:\PTO.VSK.txt

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65 gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac aac      432
66 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
67      130      135      140
69 tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac ggc      480
70 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
71 145      150      155      160
73 atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc gtg      528
74 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
75      165      170      175
77 cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc ccc      576
78 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
79      180      185      190
81 gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg agc      624
82 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
83      195      200      205
85 aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg      672
86 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
87      210      215      220
89 acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa      717
90 Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
91 225      230      235
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95 <211> LENGTH: 238
96 <212> TYPE: PRT
97 <213> ORGANISM: Aequorea victoria
99 <400> SEQUENCE: 2
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106      20      25      30
109 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
110      35      40      45
113 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
114      50      55      60
117 Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
118 65      70      75      80
121 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
122      85      90      95
125 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
126      100      105      110
129 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
130      115      120      125
133 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
134      130      135      140
137 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
138 145      150      155      160
141 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
142      165      170      175

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145 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
146          180          185          190
149 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
150          195          200          205
153 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
154          210          215          220
157 Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
158 225          230          235
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162 <211> LENGTH: 447
163 <212> TYPE: DNA
164 <213> ORGANISM: Rattus norvegicus
166 <220> FEATURE:
167 <221> NAME/KEY: CDS
168 <222> LOCATION: (1)..(444)
169 <223> OTHER INFORMATION:
172 <400> SEQUENCE: 3
173 gct gac caa ctg act gaa gag cag atc gca gaa ttc aaa gaa gct ttc      48
174 Ala Asp Gln Leu Thr Glu Glu Gln Ile Ala Glu Phe Lys Glu Ala Phe
175 1          5          10          15
177 tcc cta ttt gac aag gac ggg gat ggg aca ata aca acc aag gag ctg      96
178 Ser Leu Phe Asp Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu Leu
179          20          25          30
181 ggg acg gtg atg cgg tct ctg ggg cag aac ccc aca gaa gca gag ctg      144
182 Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu
183          35          40          45
185 cag gac atg atc aat gaa gta gat gcc gac ggt aat ggc aca atc gac      192
186 Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp
187          50          55          60
189 ttc cct gaa ttc ctg aca atg atg gca aga aaa atg aaa gac aca gac      240
190 Phe Pro Glu Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr Asp
191 65          70          75          80
193 agt gaa gaa gaa att aga gaa gcg ttc cgt gtg ttt gat aag gat ggc      288
194 Ser Glu Glu Glu Ile Arg Glu Ala Phe Arg Val Phe Asp Lys Asp Gly
195          85          90          95
197 aat ggc tac atc agt gca gca gag ctt cgc cac gtg atg aca aac ctt      336
198 Asn Gly Tyr Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu
199          100          105          110
201 gga gag aag tta aca gat gaa gag gtt gat gaa atg atc agg gaa gca      384
202 Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala
203          115          120          125
205 gac atc gat ggg gat ggt cag gta aac tac gaa gag ttt gta caa atg      432
206 Asp Ile Asp Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln Met
207          130          135          140
209 atg aca gcg aag tga      447
210 Met Thr Ala Lys
211 145
214 <210> SEQ ID NO: 4
215 <211> LENGTH: 148

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Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\02192002\I989025.raw

216 <212> TYPE: PRT
 217 <213> ORGANISM: Rattus norvegicus
 219 <400> SEQUENCE: 4
 221 Ala Asp Gln Leu Thr Glu Glu Gln Ile Ala Glu Phe Lys Glu Ala Phe
 222 1 5 10 15
 225 Ser Leu Phe Asp Lys Asp Gly Asp Gly Thr Ile Thr Thr Lys Glu Leu
 226 20 25 30
 229 Gly Thr Val Met Arg Ser Leu Gly Gln Asn Pro Thr Glu Ala Glu Leu
 230 35 40 45
 233 Gln Asp Met Ile Asn Glu Val Asp Ala Asp Gly Asn Gly Thr Ile Asp
 234 50 55 60
 237 Phe Pro Glu Phe Leu Thr Met Met Ala Arg Lys Met Lys Asp Thr Asp
 238 65 70 75 80
 241 Ser Glu Glu Glu Ile Arg Glu Ala Phe Arg Val Phe Asp Lys Asp Gly
 242 85 90 95
 245 Asn Gly Tyr Ile Ser Ala Ala Glu Leu Arg His Val Met Thr Asn Leu
 246 100 105 110
 249 Gly Glu Lys Leu Thr Asp Glu Glu Val Asp Glu Met Ile Arg Glu Ala
 250 115 120 125
 253 Asp Ile Asp Gly Asp Gly Gln Val Asn Tyr Glu Glu Phe Val Gln Met
 254 130 135 140
 257 Met Thr Ala Lys
 258 145

261 <210> SEQ ID NO: 5
 262 <211> LENGTH: 63
 263 <212> TYPE: DNA
 264 <213> ORGANISM: Artificial Sequence
 266 <220> FEATURE:
 267 <223> OTHER INFORMATION: Synthetic DNA
 269 <220> FEATURE:
 270 <221> NAME/KEY: CDS
 271 <222> LOCATION: (1)..(63)
 272 <223> OTHER INFORMATION:
 275 <400> SEQUENCE: 5

276 tca tca cgt cgt aag tgg aat aag aca ggt cac gca gtc aga gct ata 48
 277 Ser Ser Arg Arg Lys Trp Asn Lys Thr Gly His Ala Val Arg Ala Ile
 278 1 5 10 15
 280 ggt cgg ctg agc tca 63
 281 Gly Arg Leu Ser Ser
 282 20

285 <210> SEQ ID NO: 6
 286 <211> LENGTH: 21
 287 <212> TYPE: PRT
 288 <213> ORGANISM: Artificial Sequence
 290 <220> FEATURE:

291 <223> OTHER INFORMATION: Synthetic DNA
 293 <400> SEQUENCE: 6
 295 Ser Ser Arg Arg Lys Trp Asn Lys Thr Gly His Ala Val Arg Ala Ile
 296 1 5 10 15

This is an amino acid sequence, a peptide

Please correct any subsequent sequences showing the above error.

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299 Gly Arg Leu Ser Ser
300      20
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304 <211> LENGTH: 1251
305 <212> TYPE: DNA
306 <213> ORGANISM: Artificial Sequence
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Synthetic DNA
311 <220> FEATURE:
312 <221> NAME/KEY: CDS
313 <222> LOCATION: (1)..(1248)
314 <223> OTHER INFORMATION:
317 <400> SEQUENCE: 7
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320 1      5      10      15
322 aga gct ata ggt cgg ctg agc tca ctc gag aac gtc tat atc atg gcc      96
323 Arg Ala Ile Gly Arg Leu Ser Ser Leu Glu Asn Val Tyr Ile Met Ala
324      20      25      30
326 gac aag cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac      144
327 Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn
328      35      40      45
330 atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc      192
331 Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr
332      50      55      60
334 ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc      240
335 Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
336 65      70      75      80
338 acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg      288
339 Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
340      85      90      95
342 gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac      336
343 Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp
344      100      105      110
346 gag ctg tac aag ggc ggt acc gga ggg agc atg gtg agc aag ggc gag      384
347 Glu Leu Tyr Lys Gly Gly Thr Gly Gly Ser Met Val Ser Lys Gly Glu
348      115      120      125
350 gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc gac      432
351 Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
352      130      135      140
354 gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc gat gcc      480
355 Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala
356 145      150      155      160
358 acc tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag ctg      528
359 Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu
360      165      170      175
362 ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg acc tac ggc gtg cag      576
363 Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Tyr Gly Val Gln
364      180      185      190

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VERIFICATION SUMMARY

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